OIPE

RAW SEQUENCE LISTING   DATE: 11/01/2001
PATENT APPLICATION: US/09/977,406   TIME: 10:45:21

Input Set : A:\sequence-listing-ASCII-us-03.txt
Output Set: N:\CRF3\11012001\I977406.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: PROCYON BIOPHARMA INC.
W--> 5 <120> TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
W--> 6 <130> FILE REFERENCE: 06508-030-us-03
C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/977,406
C--> 7 <141> CURRENT FILING DATE: 2001-10-15
7 <150> PRIOR APPLICATION NUMBER: 2,321,256
8 <151> PRIOR FILING DATE: 2000-10-16
9 <150> PRIOR APPLICATION NUMBER: 2,355,334
10 <151> PRIOR FILING DATE: 2001-08-20
W--> 11 <160> NUMBER OF SEQ ID: 92

ERRORED SEQUENCES

E--> 13 <210> SEQ ID NO: SEQ ID NO: 1
E--> 39 <210> SEQ ID NO: SEQ ID NO: 2
E--> 67 <210> SEQ ID NO: SEQ ID NO: 3
E--> 77 <210> SEQ ID NO: SEQ ID NO: 4
E--> 87 <210> SEQ ID NO: SEQ ID NO: 5
E--> 97 <210> SEQ ID NO: SEQ ID NO: 6
E--> 110 <210> SEQ ID NO: SEQ ID NO: 7
E--> 119 <210> SEQ ID NO: SEQ ID NO:8
E--> 128 <210> SEQ ID NO: SEQ ID NO: 9
E--> 147 <210> SEQ ID NO: SEQ ID NO: 10
E--> 157 <210> SEQ ID NO: SEQ ID NO: 11
E--> 170 <210> SEQ ID NO: SEQ ID NO: 12
E--> 182 <210> SEQ ID NO: SEQ ID NO: 13
E--> 195 <210> SEQ ID NO: SEQ ID NO: 14
E--> 209 <210> SEQ ID NO: SEQ ID NO: 15
E--> 222 <210> SEQ ID NO: SEQ ID NO: 16
E--> 236 <210> SEQ ID NO: SEQ ID NO: 17
E--> 249 <210> SEQ ID NO: SEQ ID NO: 18
E--> 263 <210> SEQ ID NO: SEQ ID NO: 19
E--> 276 <210> SEQ ID NO: SEQ ID NO: 20

1363 <211> LENGTH: 15
1364 <212> TYPE: PRT *mandatory*
W--> 1365 <213> ORGANISM: *response needed*
W--> 1366 <220> FEATURE:
W--> 1367 <221> NAME/KEY: Modified site
1368 <222> LOCATION: 1
1369 <223> OTHER INFORMATION: The residue in this position is either glutamic acid, asparagine, or asparagine
1370   aspartic acid.

(This is sequence 89)

W--> 1372 <220> FEATURE:
W--> 1373 <221> NAME/KEY: Modified site
1374 <222> LOCATION: 4
1375 <223> OTHER INFORMATION: The residue in this position is either threonine, or

serine.
W--> 1377 <220> FEATURE:

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            Input Set : A:\sequence-listing-ASCII-us-03.txt
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W--> 1378 <221> NAME/KEY: Modified site
     1379 <222> LOCATION: 6
     1380 <223> OTHER INFORMATION: The residue in this position is either glutamic acid,
~~asparagin, or~~ →asparagine
     1381   aspartic acid.
W--> 1383 <220> FEATURE:
W--> 1384 <221> NAME/KEY: Modified site
     1385 <222> LOCATION: 8
     1386 <223> OTHER INFORMATION: The residue in this position is either glutamic acid,
asparagin or
     1387   aspartic acid.
W--> 1389 <220> FEATURE:
W--> 1390 <221> NAME/KEY: Modified site
     1391 <222> LOCATION: 9
     1392 <223> OTHER INFORMATION: The residue in this position is either threonine, or
serine.
W--> 1394 <220> FEATURE:
W--> 1395 <221> NAME/KEY: Modified site
     1396 <222> LOCATION: 11
     1397 <223> OTHER INFORMATION: The residue in this position is either threonine, or
serine.
W--> 1399 <220> FEATURE:
W--> 1400 <221> NAME/KEY: Modified site
     1401 <222> LOCATION: 13
     1402 <223> OTHER INFORMATION: The residue in this position is either tyrosine, or
phenylalanine.
W--> 1404 <220> FEATURE:
W--> 1405 <221> NAME/KEY: Modified site
     1406 <222> LOCATION: 14
     1407 <223> OTHER INFORMATION: The residue in this position is either glutamic acid,
asparagin, or
     1408   aspartic acid.
W--> 1410 <220> FEATURE:
W--> 1411 <221> NAME/KEY: Modified site
     1412 <222> LOCATION: 15
     1413 <223> OTHER INFORMATION: The residue in this position is either threonine, or
serine.
E--> 1415 <400> 89← insert
W--> 1416 Xaa Trp Gln Xaa Asp Xaa Cys Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa
E--> 1417 1   5   10   ~~15~~ 15

misaligned nos.

see pp 4-5

09/977,406 4

delete – do not show any alphabetical headings when using new

sequence Rules

format

```
<210> SEQ ID NO: 1
<211> 94
<212> PRT
<213>  ← mandatory response needed (see items 10
<400> 1 ← insert      and 11 on Error
                       summary sheet)
```

Ser Cys Tyr Phe Ile Pro Asn Glu Gly Val Pro Gly Asp Ser Thr Arg
 1   5   10   15

(partial listing of sequence 1)

global

error

IMPORTANT The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

delete

<210> ~~SEQ ID NO.~~ 7
<211> 26
<212> DNA
<213> ← *mandatory response*
<400> 7 ← *insert*

GGGAAGAATT CTCATGCTAT TTCATA   26

all bases must be in lower-case letters, when using new sequence rules format

Please correct all sequences showing these errors

Input Set : **A:\sequence-listing-ASCII-us-03.txt**
Output Set: **N:\CRF3\11012001\I977406.raw**

```
L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application No
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:11 M:283 W: Missing Blank Line separator, <160> field identifier
L:13 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:16 M:201 W: Mandatory field data missing, <213> ORGANISM
L:17 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:17 M:283 W: Missing Blank Line separator, <400> field identifier
L:39 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:42 M:201 W: Mandatory field data missing, <213> ORGANISM
L:43 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:43 M:283 W: Missing Blank Line separator, <400> field identifier
L:67 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:70 M:201 W: Mandatory field data missing, <213> ORGANISM
L:71 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:71 M:283 W: Missing Blank Line separator, <400> field identifier
L:77 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:80 M:201 W: Mandatory field data missing, <213> ORGANISM
L:81 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:87 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:90 M:201 W: Mandatory field data missing, <213> ORGANISM
L:91 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:91 M:283 W: Missing Blank Line separator, <400> field identifier
L:97 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:100 M:201 W: Mandatory field data missing, <213> ORGANISM
L:101 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:110 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:113 M:201 W: Mandatory field data missing, <213> ORGANISM
L:114 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:114 M:283 W: Missing Blank Line separator, <400> field identifier
L:116 M:112 C: (48) String data converted to lower case,
L:119 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:122 M:201 W: Mandatory field data missing, <213> ORGANISM
L:123 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:123 M:283 W: Missing Blank Line separator, <400> field identifier
M:112 Repeated in SeqNo=0
L:128 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:131 M:201 W: Mandatory field data missing, <213> ORGANISM
L:132 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:132 M:283 W: Missing Blank Line separator, <400> field identifier
L:147 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:150 M:201 W: Mandatory field data missing, <213> ORGANISM
L:151 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:151 M:283 W: Missing Blank Line separator, <400> field identifier
L:157 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
```

Input Set : **A:\sequence-listing-ASCII-us-03.txt**
Output Set: **N:\CRF3\11012001\I977406.raw**

```
L:160 M:201 W: Mandatory field data missing, <213> ORGANISM
L:161 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:161 M:283 W: Missing Blank Line separator, <400> field identifier
L:170 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:173 M:201 W: Mandatory field data missing, <213> ORGANISM
L:174 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:174 M:283 W: Missing Blank Line separator, <400> field identifier
L:182 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:185 M:201 W: Mandatory field data missing, <213> ORGANISM
L:186 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:186 M:283 W: Missing Blank Line separator, <400> field identifier
L:195 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:198 M:201 W: Mandatory field data missing, <213> ORGANISM
L:199 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:199 M:283 W: Missing Blank Line separator, <400> field identifier
L:209 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:212 M:201 W: Mandatory field data missing, <213> ORGANISM
L:213 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:213 M:283 W: Missing Blank Line separator, <400> field identifier
L:222 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:225 M:201 W: Mandatory field data missing, <213> ORGANISM
L:226 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:226 M:283 W: Missing Blank Line separator, <400> field identifier
L:236 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:239 M:201 W: Mandatory field data missing, <213> ORGANISM
L:240 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:240 M:283 W: Missing Blank Line separator, <400> field identifier
L:249 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:252 M:201 W: Mandatory field data missing, <213> ORGANISM
L:253 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:253 M:283 W: Missing Blank Line separator, <400> field identifier
L:263 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:266 M:201 W: Mandatory field data missing, <213> ORGANISM
L:267 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:267 M:283 W: Missing Blank Line separator, <400> field identifier
L:276 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:279 M:201 W: Mandatory field data missing, <213> ORGANISM
L:280 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:280 M:283 W: Missing Blank Line separator, <400> field identifier
L:289 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:292 M:201 W: Mandatory field data missing, <213> ORGANISM
L:293 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:293 M:283 W: Missing Blank Line separator, <400> field identifier
L:303 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:306 M:201 W: Mandatory field data missing, <213> ORGANISM
L:307 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:307 M:283 W: Missing Blank Line separator, <400> field identifier
L:316 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:319 M:201 W: Mandatory field data missing, <213> ORGANISM
```

Input Set : **A:\sequence-listing-ASCII-us-03.txt**
Output Set: **N:\CRF3\11012001\I977406.raw**

```
L:320 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:320 M:283 W: Missing Blank Line separator, <400> field identifier
L:329 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:332 M:201 W: Mandatory field data missing, <213> ORGANISM
L:333 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:333 M:283 W: Missing Blank Line separator, <400> field identifier
L:343 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:346 M:201 W: Mandatory field data missing, <213> ORGANISM
L:347 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:347 M:283 W: Missing Blank Line separator, <400> field identifier
L:360 M:201 W: Mandatory field data missing, <213> ORGANISM
L:361 M:283 W: Missing Blank Line separator, <400> field identifier
L:373 M:201 W: Mandatory field data missing, <213> ORGANISM
L:374 M:283 W: Missing Blank Line separator, <400> field identifier
L:389 M:201 W: Mandatory field data missing, <213> ORGANISM
L:390 M:283 W: Missing Blank Line separator, <400> field identifier
L:405 M:201 W: Mandatory field data missing, <213> ORGANISM
L:406 M:283 W: Missing Blank Line separator, <400> field identifier
L:421 M:201 W: Mandatory field data missing, <213> ORGANISM
L:422 M:283 W: Missing Blank Line separator, <400> field identifier
L:437 M:201 W: Mandatory field data missing, <213> ORGANISM
L:438 M:283 W: Missing Blank Line separator, <400> field identifier
L:454 M:201 W: Mandatory field data missing, <213> ORGANISM
L:455 M:283 W: Missing Blank Line separator, <400> field identifier
L:471 M:201 W: Mandatory field data missing, <213> ORGANISM
L:472 M:283 W: Missing Blank Line separator, <400> field identifier
L:487 M:201 W: Mandatory field data missing, <213> ORGANISM
L:488 M:283 W: Missing Blank Line separator, <400> field identifier
L:504 M:201 W: Mandatory field data missing, <213> ORGANISM
L:505 M:283 W: Missing Blank Line separator, <400> field identifier
L:521 M:201 W: Mandatory field data missing, <213> ORGANISM
L:522 M:283 W: Missing Blank Line separator, <400> field identifier
L:537 M:201 W: Mandatory field data missing, <213> ORGANISM
L:538 M:283 W: Missing Blank Line separator, <400> field identifier
L:553 M:201 W: Mandatory field data missing, <213> ORGANISM
L:554 M:283 W: Missing Blank Line separator, <400> field identifier
L:569 M:201 W: Mandatory field data missing, <213> ORGANISM
L:570 M:283 W: Missing Blank Line separator, <400> field identifier
L:585 M:201 W: Mandatory field data missing, <213> ORGANISM
L:586 M:283 W: Missing Blank Line separator, <400> field identifier
L:601 M:201 W: Mandatory field data missing, <213> ORGANISM
L:602 M:283 W: Missing Blank Line separator, <400> field identifier
L:617 M:201 W: Mandatory field data missing, <213> ORGANISM
L:618 M:283 W: Missing Blank Line separator, <400> field identifier
L:633 M:201 W: Mandatory field data missing, <213> ORGANISM
L:634 M:283 W: Missing Blank Line separator, <400> field identifier
L:653 M:201 W: Mandatory field data missing, <213> ORGANISM
L:654 M:283 W: Missing Blank Line separator, <400> field identifier
L:672 M:201 W: Mandatory field data missing, <213> ORGANISM
```

Input Set : **A:\sequence-listing-ASCII-us-03.txt**
Output Set: **N:\CRF3\11012001\I977406.raw**

L:673 M:283 W: Missing Blank Line separator, <400> field identifier
L:691 M:201 W: Mandatory field data missing, <213> ORGANISM
L:692 M:283 W: Missing Blank Line separator, <400> field identifier
L:710 M:201 W: Mandatory field data missing, <213> ORGANISM
L:711 M:283 W: Missing Blank Line separator, <400> field identifier
L:729 M:201 W: Mandatory field data missing, <213> ORGANISM
L:748 M:201 W: Mandatory field data missing, <213> ORGANISM
L:767 M:201 W: Mandatory field data missing, <213> ORGANISM
L:1367 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1373 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1378 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1384 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1390 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1395 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1400 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1405 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1411 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:0
L:1416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1417 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0

**ERROR DETECTED**   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/977,406_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOF

1____Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2____Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

· 3____Misaligned Amino Numbering — The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences (OLD RULES) — Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences (NEW RULES) — Sequence(s)_____ missing. If Intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Response _FYI_ — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220> _FYI_ — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n — n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.
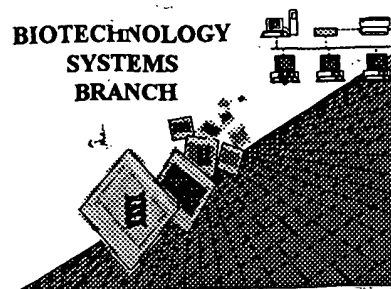
RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/977,406_

Source: _OIPE_

Date Processed by STIC: _11/1/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker